

1645

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0280

01PE

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 10/027,450

CRF Processing Date: 1/22/2002

Edited by:

Verified by:

(STIC staff)

ENTERED

☐ Changed a file from non-ASCII to ASCII☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.☐ Edited a format error in the Current Application Data section, specifically:☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____☐ Added the mandatory heading and subheadings for "Current Application Data".☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.☐ Inserted colons after headings/subheadings. Headings edited included:☐ Deleted extra, invalid, headings used by an applicant, specifically:☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____☐ Inserted mandatory headings, specifically: _____☒ Corrected an obvious error in the response, specifically:☐ Edited identifiers where upper case is used but lower case is required, or vice versa.☐ Corrected an error in the Number of Sequences field, specifically:☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____☐ Other: _____

TECH CENTER 1600/2900

FEB 21 2002

RECEIVED

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPÉ

RAW SEQUENCE LISTING

DATE: 01/22/2002

PATENT APPLICATION: US/10/027,450

TIME: 19:35:36

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01222002\J027450.raw

```

3 <110> APPLICANT: Falco, Saverio Carl
4      Hitz, William D.
5      Kinney, Anthony J.
6      Cahoon, Rebecca E.
7      Rafalski, J. Antoni
9 <120> TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
11 <130> FILE REFERENCE: BB-1126
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/027,450
C--> 14 <141> CURRENT FILING DATE: 2001-12-20
16 <150> PRIOR APPLICATION NUMBER: 60/063,423
17 <151> PRIOR FILING DATE: 1997-10-28
19 <160> NUMBER OF SEQ ID NOS: 54
21 <170> SOFTWARE: Microsoft Word Version 7.0A
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2135
25 <212> TYPE: DNA
26 <213> ORGANISM: Zea mays
28 <400> SEQUENCE: 1
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30 acccaaaacc ctaaacccca ttccgtacct caacgccgcc gccgccgccg ccgccgctgc 120
31 gatgcagtcc atggcgctca cctcccctc actcccgag gtcggcccg tttccggccg 180
32 ccgtctccag cgcacccgtg ccaccgcgg atccgacgag ctcaagctga acaagtacag 240
33 cgcgcgcata cgggagccca agtcgcagg cgcctcgcag gccgtgctct atggggtcgg 300
34 gctcactgac gctgacctcc gcaagccga ggtcggcgct tcgtcgggtg ggtacgaggg 360
35 gaacacctgc aacatgcacc tgctccgcct cgcggaggcc gtccgtgacg gcgtccgcga 420
36 ggccggcatg atcggcttcc ggtttaacac cgtcgggtgc agcgacgcca ttccatggg 480
37 caccgggggc atgtgctaca gctccagtc ccgtgacctc atcgccgaca gcatcgagac 540
38 cgtcatggga gcgcagcact acgacgccaa catttccata cctgggtgcg acaagaacat 600
39 gccaggtaca ataattggaa tgggacggct taatcgacct agcataatga tatatggtgg 660
40 aactattaag cctgggtcact ttccaggcaa ttccatgat atagtatctg ctttccagtg 720
41 ctatggagaa tatgttagtg gttcaatcac tgatgagcaa agaaagaacg tcctccgcaa 780
42 ttcatgtcca ggagcagggt cctgtggtgg tatgtacaca gcaaacacta tggcatctgc 840
43 tatcgaaact ttgggcatga gtcttccata cagttcttcg acacctgctg aggaccact 900
44 aaaactagaa gagtgcgctc ttgctgggaa gtatctttta gatttgctaa agatggattt 960
45 gaagcctaag gacattatca ctgagaagtc attgcgaaat gcaatggtta ttgttatggc 1020
46 acttggtggt tcgactaatg ctgtttctgca ttgtattgcc attgtcgggt ccgttggttt 1080
47 gcatttgact cttgatgatt tccagaaggc cagtgaacca gttcctttcc ttgcagacct 1140
48 caagcccagt ggcaaatatg tcatggagga tctacataag attggtggga cacctgcagt 1200
49 cattcattac cttttggagc aaggtcttct tgatggtgat tgcagtactg ttactggtaa 1260
50 aactctagct gagaatgcta aaatcttccc tcctctgtct gaggggcagc aaataattcg 1320
51 accacttgac aatcctatca aaccaactgg ccatattcaa atactttatg gaaatcttgc 1380
52 accggaaggc tctgtcgcaa aaataactgg caaagaggga ctgttcttct caggtcccg 1440
53 attagttttt gaggggtgaag aatccatgat cacagctatc tcagaaaacc cagcgaattt 1500

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55 aatgttgact ccaacaagtg caataatggg tgctggtctc ggaaaggagt gcgccctgct 1620
56 gacagatggt agattttcag gaggctcaca tggatttgtt gtcggccaca tatgccctga 1680
57 agcacaggaa ggtggcccga ttggccttgt ccatagtggg gatgtaatca ccatcgatgt 1740
58 aagtaagagg gtaatcgacg ttgaccttac cgagcagcag ctcgaagaaa gacggaggaa 1800
59 atggacccca ccgccataca agtccacctg tggagctctt tggaagtaca tcaagcttgt 1860
60 ggctccagcg tctagaggat gcgtcactga tgagtaggat gtgttacatt ctgttaggtt 1920
61 gtgcacatga tgtgtttgtc aatcaaaagc tgttgccagg aacaatttcc ctgttagagt 1980
62 gattcattgt agttcggttt tgcatgtggc aggtatgaca ataaattgcc ggtttctaag 2040
63 agcttagcaa tgctgcagaa actgctgaat aatcgagtgt aatcgggggc cgtgagcaat 2100
64 cacatctttg tcagtcaaaa aaaaaaaaaa aaaaaa 2135
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67 <211> LENGTH: 591
68 <212> TYPE: PRT
69 <213> ORGANISM: Zea mays
71 <400> SEQUENCE: 2
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73 1 5 10 15
75 Val Ser Gly Arg Arg Leu Gln Arg Ile Arg Ala Thr Ala Val Ser Asp
76 20 25 30
78 Glu Leu Lys Leu Asn Lys Tyr Ser Ala Arg Ile Thr Glu Pro Lys Ser
79 35 40 45
81 Gln Gly Ala Ser Gln Ala Val Leu Tyr Gly Val Gly Leu Thr Asp Ala
82 50 55 60
84 Asp Leu Arg Lys Pro Gln Val Gly Val Ser Ser Val Trp Tyr Glu Gly
85 65 70 75 80
87 Asn Thr Cys Asn Met His Leu Leu Arg Leu Ala Glu Ala Val Arg Asp
88 85 90 95
90 Gly Val Arg Glu Ala Gly Met Val Gly Phe Arg Phe Asn Thr Val Gly
91 100 105 110
93 Val Ser Asp Ala Ile Ser Met Gly Thr Arg Gly Met Cys Tyr Ser Leu
94 115 120 125
96 Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val Met Gly Ala
97 130 135 140
99 Gln His Tyr Asp Ala Asn Ile Ser Ile Pro Gly Cys Asp Lys Asn Met
100 145 150 155 160
102 Pro Gly Thr Ile Met Ala Met Gly Arg Leu Asn Arg Pro Ser Ile Met
103 165 170 175
105 Ile Tyr Gly Gly Thr Ile Lys Pro Gly His Phe Gln Gly Asn Ser Tyr
106 180 185 190
108 Asp Ile Val Ser Ala Phe Gln Cys Tyr Gly Glu Tyr Val Ser Gly Ser
109 195 200 205
111 Ile Thr Asp Glu Gln Arg Lys Asn Val Leu Arg Asn Ser Cys Pro Gly
112 210 215 220
114 Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala
115 225 230 235 240
117 Ile Glu Thr Leu Gly Met Ser Leu Pro Tyr Ser Ser Ser Thr Pro Ala
118 245 250 255
120 Glu Asp Pro Leu Lys Leu Glu Glu Cys Arg Leu Ala Gly Lys Tyr Leu

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01222002\J027450.raw

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121          260          265          270
123 Leu Glu Leu Leu Lys Met Asp Leu Lys Pro Lys Asp Ile Ile Thr Glu
124          275          280          285
126 Lys Ser Leu Arg Asn Ala Met Val Ile Val Met Ala Leu Gly Gly Ser
127          290          295          300
129 Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Arg Ser Val Gly Leu
130 305          310          315          320
132 His Leu Thr Leu Asp Asp Phe Gln Lys Val Ser Asp Gln Val Pro Phe
133          325          330          335
135 Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Glu Asp Leu His
136          340          345          350
138 Lys Ile Gly Gly Thr Pro Ala Val Ile His Tyr Leu Leu Glu Gln Gly
139          355          360          365
141 Leu Leu Asp Gly Asp Cys Met Thr Val Thr Gly Lys Thr Leu Ala Glu
142          370          375          380
144 Asn Ala Lys Ile Phe Pro Pro Leu Ser Glu Gly Gln Gln Ile Ile Arg
145 385          390          395          400
147 Pro Leu Asp Asn Pro Ile Lys Pro Thr Gly His Ile Gln Ile Leu Tyr
148          405          410          415
150 Gly Asn Leu Ala Pro Glu Gly Ser Val Ala Lys Ile Thr Gly Lys Glu
151          420          425          430
153 Gly Leu Phe Phe Ser Gly Pro Ala Leu Val Phe Glu Gly Glu Glu Ser
154          435          440          445
156 Met Ile Thr Ala Ile Ser Glu Asn Pro Ala Asn Phe Lys Gly Lys Val
157          450          455          460
159 Val Val Ile Arg Gly Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu
160 465          470          475          480
162 Met Leu Thr Pro Thr Ser Ala Ile Met Gly Ala Gly Leu Gly Lys Glu
163          485          490          495
165 Cys Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe
166          500          505          510
168 Val Val Gly His Ile Cys Pro Glu Ala Gln Glu Gly Gly Pro Ile Gly
169          515          520          525
171 Leu Val His Ser Gly Asp Val Ile Thr Ile Asp Val Ser Lys Arg Val
172          530          535          540
174 Ile Asp Val Asp Leu Thr Glu Gln Gln Leu Glu Glu Arg Arg Arg Lys
175 545          550          555          560
177 Trp Thr Pro Pro Pro Tyr Lys Ser Thr Cys Gly Ala Leu Trp Lys Tyr
178          565          570          575
180 Ile Lys Leu Val Ala Pro Ala Ser Arg Gly Cys Val Thr Asp Glu
181          580          585          590
183 <210> SEQ ID NO: 3
184 <211> LENGTH: 2073
185 <212> TYPE: DNA
186 <213> ORGANISM: Glycine max
188 <400> SEQUENCE: 3
189 gtaaaccctt ttccatcta gagttgttgc ggctctcttc tctgcacact cagaatgcag 60
190 tccacactct tcaacccac ccattccctt atccccactt caccacactc tatcagatcc 120
191 aattctggtc atgtttctct ctccgttcgc gctccatcg ccgtggaaac ccccacggag 180

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01222002\J027450.raw

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192 acggtgaagc tgaacaagta cagctcccg c atcaccgagc ccaaatcgca gggcgccctcc 240
193 caggccgtgc tctacggcgt cggctctctcc gaggacgaca tggccaagcc ccagggtcggc 300
194 gtctcctcgg tctggtagca gggcaacacc tgcaacatgc acctcctcca cctctccgag 360
195 gccgtgcgtg acggcggttg tgctgctggc atggttccct tccgcttcaa caccggttggc 420
196 gtcagcgacg ccatctccat gggcaccggt ggcattgtgt acagcctcca gtccagggac 480
197 ctcatgtccg acagcatcga gaccgtcatg gcagcgcagt ggtacgatgg caatatttcc 540
198 atccccggct gtgacaaaaa tatgccaggt actatcattg ccatggggag gctcaacaga 600
199 cctagcatta tggtttatgg cgggactata aaacctggtc attttgaggg taacacgttt 660
200 gacatagtgt ctgcctttca gtgctatgga gaatatgtga gtggatcaat taatgatgac 720
201 caaagacaaa atgttattcg caactcatgc cctggggctg gagcctgtgg tggaatgtat 780
202 acagccaata ccatggcttc tgcaatagaa gctatgggaa tgtctcttcc ctatagctca 840
203 tctacacctg ctgaggatcc actaaagtgt gatgagtgtc gtttagctgg gaaatatctt 900
204 cttgagttac tgaatatgga cttgaagccc cgagatatca tcaactcgtaa atcaactacgt 960
205 aatgcaatgg ttatagttat ggcacttggg ggatctacta atgctgtgtt acatttaatt 1020
206 gctattgcc aagtctgttg cattgatttg actcttgatg attttcagaa ggtagcgat 1080
207 gaggttcctt ttattgcaga tcttaagcct agtgggaaat atgtcatgga agatgttcac 1140
208 aagattggag ggactcctgc agttatccgc taccttcttg agcaaggctt tttagatggg 1200
209 gactgtatga ctgtcactgg aaaaacccta gctgaaaatg cagaacttgt ccctcctctg 1260
210 tccaacgggc aggaaataat aaggccagta gaaaatccca tcaagaagac ggctcacatt 1320
211 caaatattat atggaaacct tgcaccacag ggttccggtt ctaaaattac tggaaaagaa 1380
212 gggctgtact tctctgttcc tgcacttgtc tttgaaggag aggaggcaat gattgctgcc 1440
213 atttcagagg atccttcgag ttttaagggg aaagtgggtt taatcagggg agagggaccc 1500
214 aaggggtggtc cggaatgcc tgagatgtta acaccaacaa gtgcaataat ggggtgcagg 1560
215 cttggaaagg aagtgcatt attgactgat ggaagatttt caggagggtc acatggattt 1620
216 gtggttggtc atatatgtcc tgaagcacag gaaggtggtc caattggctt gattcaaaat 1680
217 ggagacgtaa tcaatgttga catcaagaat aggagaattg atgttttggg atcagatgag 1740
218 gagatggaag cacgcaggaa aaagtggact gctcctccat acaaagctaa ccgaggagct 1800
219 ctgtacaagt atattaaaaa tgtgacacct gcttctagtg gatgcgtaac agacgagtag 1860
220 aaagacatac ctgcagagca aaagctgata gtatgccttg gtgaaatttt gtcttggttt 1920
221 tccagaacaa gttggtaaaa attcaaaaac aaacctcatt tcagagaatt taaaacaatg 1980
222 gaattgaatt gctactattg attagtgact atttaattat tatgattttc tagagctaaa 2040
223 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2073

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225 <210> SEQ ID NO: 4

226 <211> LENGTH: 601

227 <212> TYPE: PRT

228 <213> ORGANISM: Glycine max

230 <400> SEQUENCE: 4

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231 Met Gln Ser Thr Leu Phe Asn Pro Thr His Ser Leu Ile Pro Thr Ser
232 1 5 10 15
234 Pro His Ser Ile Arg Ser Asn Ser Gly His Ala Ser Leu Ser Val Arg
235 20 25 30
237 Ala Ser Ile Ala Val Glu Thr Pro Thr Glu Thr Val Lys Leu Asn Lys
238 35 40 45
240 Tyr Ser Ser Arg Ile Thr Glu Pro Lys Ser Gln Gly Ala Ser Gln Ala
241 50 55 60
243 Val Leu Tyr Gly Val Gly Leu Ser Glu Asp Asp Met Ala Lys Pro Gln
244 65 70 75 80
246 Val Gly Val Ser Ser Val Trp Tyr Glu Gly Asn Thr Cys Asn Met His
247 85 90 95

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Input Set : A:\PTO.AMC.txt

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249 Leu Leu His Leu Ser Glu Ala Val Arg Asp Gly Val Ala Ala Ala Gly
250      100      105      110
252 Met Val Pro Phe Arg Phe Asn Thr Val Gly Val Ser Asp Ala Ile Ser
253      115      120      125
255 Met Gly Thr Arg Gly Met Cys Tyr Ser Leu Gln Ser Arg Asp Leu Ile
256      130      135      140
258 Ala Asp Ser Ile Glu Thr Val Met Ala Ala Gln Trp Tyr Asp Gly Asn
259 145      150      155      160
261 Ile Ser Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Thr Ile Ile Ala
262      165      170      175
264 Met Gly Arg Leu Asn Arg Pro Ser Ile Met Val Tyr Gly Gly Thr Ile
265      180      185      190
267 Lys Pro Gly His Phe Glu Gly Asn Thr Phe Asp Ile Val Ser Ala Phe
268      195      200      205
270 Gln Cys Tyr Gly Glu Tyr Val Ser Gly Ser Ile Asn Asp Asp Gln Arg
271      210      215      220
273 Gln Asn Val Ile Arg Asn Ser Cys Pro Gly Ala Gly Ala Cys Gly Gly
274 225      230      235      240
276 Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Ala Met Gly Met
277      245      250      255
279 Ser Leu Pro Tyr Ser Ser Ser Thr Pro Ala Glu Asp Pro Leu Lys Leu
280      260      265      270
282 Asp Glu Cys Arg Leu Ala Gly Lys Tyr Leu Leu Glu Leu Leu Lys Met
283      275      280      285
285 Asp Leu Lys Pro Arg Asp Ile Ile Thr Arg Lys Ser Leu Arg Asn Ala
286      290      295      300
288 Met Val Ile Val Met Ala Leu Gly Gly Ser Thr Asn Ala Val Leu His
289 305      310      315      320
291 Leu Ile Ala Ile Ala Lys Ser Val Gly Ile Asp Leu Thr Leu Asp Asp
292      325      330      335
294 Phe Gln Lys Val Ser Asp Glu Val Pro Phe Ile Ala Asp Leu Lys Pro
295      340      345      350
297 Ser Gly Lys Tyr Val Met Glu Asp Val His Lys Ile Gly Gly Thr Pro
298      355      360      365
300 Ala Val Ile Arg Tyr Leu Leu Glu Gln Gly Phe Leu Asp Gly Asp Cys
301      370      375      380
303 Met Thr Val Thr Gly Lys Thr Leu Ala Glu Asn Ala Glu Leu Val Pro
304 385      390      395      400
306 Pro Leu Ser Asn Gly Gln Glu Ile Ile Arg Pro Val Glu Asn Pro Ile
307      405      410      415
309 Lys Lys Thr Ala His Ile Gln Ile Leu Tyr Gly Asn Leu Ala Pro Gln
310      420      425      430
312 Gly Ser Val Ala Lys Ile Thr Gly Lys Glu Gly Leu Tyr Phe Ser Gly
313      435      440      445
315 Pro Ala Leu Val Phe Glu Gly Glu Glu Ala Met Ile Ala Ala Ile Ser
316      450      455      460
318 Glu Asp Pro Ser Ser Phe Lys Gly Lys Val Val Val Ile Arg Gly Glu
319 465      470      475      480
321 Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Thr Pro Thr Ser

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/027,450

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Input Set : A:\PTO.AMC.txt

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L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:362 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:402 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:694 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:695 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:696 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:697 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:697 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:731 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1844 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:37
L:1844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1976 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39
L:1976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1977 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39
L:1977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1978 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39
L:1978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:1979 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39
L:1979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:2009 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:40
L:2009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:2061 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:42
L:2061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:2416 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
L:2416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51